

#5

OIPE

## RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/775,181

DATE: 07/19/2001

TIME: 12:02:41

Input Set : A:\LEX-0129-USA SEQLIST.txt  
 Output Set: N:\CRF3\07192001\I775181.raw

4 <110> APPLICANT: Donoho, Gregory  
 5 Hilbun, Erin  
 7 <120> TITLE OF INVENTION: Novel Human Membrane Proteins and  
 8 Polynucleotides Encoding the Same  
 11 <130> FILE REFERENCE: LEX-0129-USA  
 C--> 13 <140> CURRENT APPLICATION NUMBER: US/09/775,181  
 C--> 13 <141> CURRENT FILING DATE: 2001-02-01  
 13 <150> PRIOR APPLICATION NUMBER: US 60/180,414  
 14 <151> PRIOR FILING DATE: 2000-02-04  
 16 <160> NUMBER OF SEQ ID NOS: 5  
 18 <170> SOFTWARE: FastSEQ for Windows Version 4.0  
 20 <210> SEQ ID NO: 1  
 21 <211> LENGTH: 3648  
 22 <212> TYPE: DNA  
 23 <213> ORGANISM: Homo sapiens  
 25 <400> SEQUENCE: 1

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27 gcttgtggcg	ccagccgcga	cccccaagga	cggccggatt	cccctcgaga	gaggaccccg	120
28 aaggggaaagc	cgcacgccc	gcagccgggt	cgagcctctg	cctcggactc	ctcgctccc	180
29 tggagccgct	ccaccatgg	caccatcttg	gcgcagaaac	tcgcccggaga	gttgcggcatg	240
30 gacgtggcct	cttacacctta	caccggggac	tcccaccage	tgaagcgagc	caactgctcc	300
31 ggccgctacg	atgtggcggg	cctgccccgg	aagtggccag	ccctggccag	cgcgcaccc	360
32 tccttgcacc	gggcgcgttga	cacactgaca	cacgcacca	acttccctcaa	cgtgatgctg	420
33 cagagaata	agtgcggga	gcagaacttg	caggacgacc	tggattggta	ccagcgcgtg	480
34 gtgtggagcc	ttctggaggg	cgagcccagg	atctcccggt	cgcccatc	ttcagcacc	540
35 gattcgtgt	ccgcaccggc	cccacagggtc	ttcctccagg	ccacgcgcga	ggagagccgc	600
36 atccctgtcc	aagacctgtc	ctccctccgca	ccccacctgg	ccaacgcac	tctggagacc	660
37 gagttgttcc	acggcctccg	gycgaagtgg	aggccccact	tacaccgcg	cgcccccaat	720
38 caggggcccc	ggggcctggg	ccacagctgg	cggcgaagg	acgggctcgg	cggggacaag	780
39 agccacttca	agtggcttcc	gccttatctg	gagtgcgaga	acgggagttt	caagccccgg	840
40 tggctggtta	ctctttctc	tgcacatctac	gggttgcagc	ctaaccctgt	cccggaaattc	900
41 aggggtgtca	tgaaaagtta	cataaatctt	cagaaaagtgg	acattgacca	atgctcaagt	960
42 gatggcttgt	tttcaggaaac	tcataaaatgc	caccccaaca	attcagagtg	tatgccaatt	1020
43 aaaggcttag	gattcgttct	tggagcctat	gagtgcattt	gcaaaaggcagg	attctatcat	1080
44 cctggagttct	taccatgttca	caactttcgg	agaaggggtc	cggatcagca	tatttcagga	1140
45 agtacaaaag	atgtgtcaga	agaaggctat	gtctgcctac	tttgcaggg	gggctggccc	1200
46 ttctgtgt	atgacagccc	atgcttcgtc	caggaagata	agtatttacg	acttgcac	1260
47 atcccttcc	aaggcctgt	tatgtctgtc	gacttcgtt	gcatgcttgt	ggtctaccac	1320
48 ttctgcataag	caaagagcat	ccgggcac	ggccttatcc	tgttggaaac	gatcccttt	1380
49 ggatctctgc	tcctataactt	tccagttgtt	attttgtact	ttgagccaag	cacatttcgc	1440
50 tgtattctcc	taagatgggc	tcgtcttctc	ggttttgtca	ctgtttacgg	aactgtca	1500
51 ctcaaacttca	acagggtttt	gaagggtgtt	cttacacgaa	cggctcaac	aattccatat	1560
52 atgactggcg	gacgggtcat	gaggatgtctg	gcagtaatac	tcttggtagt	gttttgggtt	1620
53 ctcatggct	ggacttcatc	tgtgtgccag	aatttggaga	aacagatttc	acttattggc	1680
54 cagggaaaaa	catccgatca	cctcatctc	aatatgtgcc	tcattgaccc	ctgggactac	1740
55 atgacagcag	ttgctgaatt	tttattctc	ttgtgggtt	tttatctctg	ctatgcagt	1800
56 cggacagtc	catccgatc	ccatgagccc	cgctatatgg	ctgttgca	tcacaatgag	1860

ENTERED

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58	gattggatgt	tgtatgttgcacat	actcatttga	ctgtgacagt	caccattggg		1980
59	ttgttttga	ttccaaagtt	ttcacattca	agaataacc	cacgagatga	tattgctaca	2040
60	gaagcatatg	aggatgagct	agacatgggc	cgatctggat	cctacctgaa	cagcagtatc	2100
61	aattcagcct	ggagttagca	cagcttggat	ccagaggaca	ttcgggacga	gctgaaaaaa	2160
62	ctctatgccc	aactggaaat	atataaaaga	aagaagatga	tcacaaacaa	cccccacctc	2220
63	cagaaaaaagc	ggtgctcgaa	gaagggccta	ggtcgttcca	tcatgagacg	cattacggag	2280
64	atcccagaga	cagtccggc	gcagtgtctt	aaagaggaca	aggagggcgc	cgaccatggc	2340
65	acagccaaag	gcactccct	catcaggaag	aaccccccag	agtcttcagg	gaacacaggg	2400
66	aaatccaagg	aggagaccct	gaaaaaccga	gtcttcac	tcaagaaatc	ccacagcact	2460
67	tatgaccacg	tgagagacca	aacggaaagag	tccagtagcc	tacccacaga	aagccaagag	2520
68	gaggagacaa	cagaaaattc	cacactggaa	tccctgtcgg	gtaaaaaaact	aacacaaaaa	2580
69	ctaaaagaag	acagcgagc	tgagtccacg	gagtcggtgc	cgttggtgtg	caagtcagca	2640
70	agcgtcaca	acctcagctc	agagaagaaa	actggcacc	cacgaacatc	gatgttacag	2700
71	aagtctctca	gtgtcatagc	aagcgccaag	gagaagactc	ttggattagc	tggaaaaacc	2760
72	caaacagcag	gtgtgaaaga	acgcactaaa	tcccagaaac	ctttgccaaa	agataaagag	2820
73	acaaacagaa	atcactcaa	ttctgataac	acagagacta	aagatcctc	cccccaaaac	2880
74	tcaaatcctg	cgaggagcc	aagaaagcct	cagaatctg	gattatgaa	acaacaaagg	2940
75	gtcaacccca	ccactgccaa	ttctgacctg	aacccaggca	ccacccagat	gaaggacaac	3000
76	tttgacattg	gggaggtgt	tccttggag	gtttatgacc	tgacccctgg	tcctgtgcct	3060
77	tcagaatcaa	aagttcaaaa	gcacgtatct	attgtggctt	ctgaaatgga	gaaaaacccc	3120
78	acttttcct	taaaggagaa	atctcaccac	aagcctaagg	cagctgaggt	ttgtcagcaa	3180
79	tccaaatcaga	agcgcata	taaggctgaa	gtatgcctt	gggagagcca	aggccagtc	3240
80	attttgaaag	atgagaagct	tttgatttcc	aagactccag	ttctcccaga	gaggcaaaa	3300
81	gaggagaacg	gaggtcagcc	tctgcagcc	aatgtgtgt	ctgggcagag	cgaagaactg	3360
82	ccccccaaag	ctgtacatc	aaaaacagag	aatgaaaatc	tcaaccaa	aggacaccag	3420
83	gaaaaaaaaa	catcttcttc	tgaggagaat	gtgcgtggct	cctataactc	aagtaataac	3480
84	ttccagcaac	ctttaacatc	acgagcagag	gtttgtcctt	gggagtttga	gacccagct	3540
85	caaccaaatg	ctggaagaag	tgtagcttta	cctgccttct	ctgctctaag	tgcaaataag	3600
86	atacgagggc	cttagaaaga	agagatctgg	gatagttta	aagtgttag		3648

88 <210> SEQ ID NO: 2

89 <211> LENGTH: 1215

90 <212> TYPE: PRT

91 <213> ORGANISM: Homo sapiens

93 <400> SEQUENCE: 2

94	Met	Gly	Ala	Met	Ala	Tyr	Pro	Leu	Leu	Leu	Cys	Leu	Leu	Leu	Ala	Gln
95	1			5				10				15				
96	Leu	Gly	Leu	Gly	Ala	Val	Gly	Ala	Ser	Arg	Asp	Pro	Gln	Gly	Arg	Pro
97				20				25				30				
98	Asp	Ser	Pro	Arg	Glu	Arg	Thr	Pro	Lys	Gly	Lys	Pro	His	Ala	Gln	Gln
99				35				40				45				
100	Pro	Gly	Arg	Ala	Ser	Ala	Ser	Asp	Ser	Ser	Ala	Pro	Trp	Ser	Arg	Ser
101				50				55				60				
102	Thr	Asp	Gly	Thr	Ile	Leu	Ala	Gln	Lys	Leu	Ala	Glu	Glu	Val	Pro	Met
103	65				70				75				80			
104	Asp	Val	Ala	Ser	Tyr	Leu	Tyr	Thr	Gly	Asp	Ser	His	Gln	Leu	Lys	Arg
105					85				90				95			
106	Ala	Asn	Cys	Ser	Gly	Arg	Tyr	Glu	Leu	Ala	Gly	Leu	Pro	Gly	Lys	Trp
107					100				105				110			

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108 Pro Ala Leu Ala Ser Ala His Pro Ser Leu His Arg Ala Leu Asp Thr  
109 115 120 125  
110 Leu Thr His Ala Thr Asn Phe Leu Asn Val Met Leu Gln Ser Asn Lys  
111 130 135 140  
112 Ser Arg Glu Gln Asn Leu Gln Asp Asp Leu Asp Trp Tyr Gln Ala Leu  
113 145 150 155 160  
114 Val Trp Ser Leu Leu Glu Gly Glu Pro Ser Ile Ser Arg Ala Ala Ile  
115 165 170 175  
116 Thr Phe Ser Thr Asp Ser Leu Ser Ala Pro Ala Pro Gln Val Phe Leu  
117 180 185 190  
118 Gln Ala Thr Arg Glu Glu Ser Arg Ile Leu Leu Gln Asp Leu Ser Ser  
119 195 200 205  
120 Ser Ala Pro His Leu Ala Asn Ala Thr Leu Glu Thr Glu Trp Phe His  
121 210 215 220  
122 Gly Leu Arg Arg Lys Trp Arg Pro His Leu His Arg Arg Gly Pro Asn  
123 225 230 235 240  
124 Gln Gly Pro Arg Gly Leu Gly His Ser Trp Arg Arg Lys Asp Gly Leu  
125 245 250 255  
126 Gly Gly Asp Lys Ser His Phe Lys Trp Ser Pro Pro Tyr Leu Glu Cys  
127 260 265 270  
128 Glu Asn Gly Ser Tyr Lys Pro Gly Trp Leu Val Thr Leu Ser Ser Ala  
129 275 280 285  
130 Ile Tyr Gly Leu Gln Pro Asn Leu Val Pro Glu Phe Arg Gly Val Met  
131 290 295 300  
132 Lys Val Asp Ile Asn Leu Gln Lys Val Asp Ile Asp Gln Cys Ser Ser  
133 305 310 315 320  
134 Asp Gly Trp Phe Ser Gly Thr His Lys Cys His Leu Asn Asn Ser Glu  
135 325 330 335  
136 Cys Met Pro Ile Lys Gly Leu Gly Phe Val Leu Gly Ala Tyr Glu Cys  
137 340 345 350  
138 Ile Cys Lys Ala Gly Phe Tyr His Pro Gly Val Leu Pro Val Asn Asn  
139 355 360 365  
140 Phe Arg Arg Arg Gly Pro Asp Gln His Ile Ser Gly Ser Thr Lys Asp  
141 370 375 380  
142 Val Ser Glu Glu Ala Tyr Val Cys Leu Pro Cys Arg Glu Gly Cys Pro  
143 385 390 395 400  
144 Phe Cys Ala Asp Asp Ser Pro Cys Phe Val Gln Glu Asp Lys Tyr Leu  
145 405 410 415  
146 Arg Leu Ala Ile Ile Ser Phe Gln Gly Leu Cys Met Leu Leu Asp Phe  
147 420 425 430  
148 Val Ser Met Leu Val Val Tyr His Phe Arg Lys Ala Lys Ser Ile Arg  
149 435 440 445  
150 Ala Ser Gly Leu Ile Leu Leu Glu Thr Ile Leu Phe Gly Ser Leu Leu  
151 450 455 460  
152 Leu Tyr Phe Pro Val Val Ile Leu Tyr Phe Glu Pro Ser Thr Phe Arg  
153 465 470 475 480  
154 Cys Ile Leu Leu Arg Trp Ala Arg Leu Leu Gly Phe Ala Thr Val Tyr  
155 485 490 495  
156 Gly Thr Val Thr Leu Lys Leu His Arg Val Leu Lys Val Phe Leu Ser

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157	500	505	510
158	Arg Thr Ala Gln Arg Ile Pro Tyr Met Thr Gly Gly Arg Val Met Arg		
159	515	520	525
160	Met Leu Ala Val Ile Leu Leu Val Val Phe Trp Phe Leu Ile Gly Trp		
161	530	535	540
162	Thr Ser Ser Val Cys Gln Asn Leu Glu Lys Gln Ile Ser Leu Ile Gly		
163	545	550	555
164	Gln Gly Lys Thr Ser Asp His Leu Ile Phe Asn Met Cys Leu Ile Asp		
165	565	570	575
166	Arg Trp Asp Tyr Met Thr Ala Val Ala Glu Phe Leu Phe Leu Leu Trp		
167	580	585	590
168	Gly Val Tyr Leu Cys Tyr Ala Val Arg Thr Val Pro Ser Ala Phe His		
169	595	600	605
170	Glu Pro Arg Tyr Met Ala Val Ala Val His Asn Glu Leu Ile Ile Ser		
171	610	615	620
172	Ala Ile Phe His Thr Ile Arg Phe Val Leu Ala Ser Arg Leu Gln Ser		
173	625	630	635
174	Asp Trp Met Leu Met Leu Tyr Phe Ala His Thr His Leu Thr Val Thr		
175	645	650	655
176	Val Thr Ile Gly Leu Leu Leu Ile Pro Lys Phe Ser His Ser Ser Asn		
177	660	665	670
178	Asn Pro Arg Asp Asp Ile Ala Thr Glu Ala Tyr Glu Asp Glu Leu Asp		
179	675	680	685
180	Met Gly Arg Ser Gly Ser Tyr Leu Asn Ser Ser Ile Asn Ser Ala Trp		
181	690	695	700
182	Ser Glu His Ser Leu Asp Pro Glu Asp Ile Arg Asp Glu Leu Lys Lys		
183	705	710	715
184	Leu Tyr Ala Gln Leu Glu Ile Tyr Lys Arg Lys Lys Met Ile Thr Asn		
185	725	730	735
186	Asn Pro His Leu Gln Lys Lys Arg Cys Ser Lys Lys Gly Leu Gly Arg		
187	740	745	750
188	Ser Ile Met Arg Arg Ile Thr Glu Ile Pro Glu Thr Val Ser Arg Gln		
189	755	760	765
190	Cys Ser Lys Glu Asp Lys Glu Gly Ala Asp His Gly Thr Ala Lys Gly		
191	770	775	780
192	Thr Ala Leu Ile Arg Lys Asn Pro Pro Glu Ser Ser Gly Asn Thr Gly		
193	785	790	795
194	Lys Ser Lys Glu Glu Thr Leu Lys Asn Arg Val Phe Ser Leu Lys Lys		
195	805	810	815
196	Ser His Ser Thr Tyr Asp His Val Arg Asp Gln Thr Glu Glu Ser Ser		
197	820	825	830
198	Ser Leu Pro Thr Glu Ser Gln Glu Glu Glu Thr Thr Glu Asn Ser Thr		
199	835	840	845
200	Leu Glu Ser Leu Ser Gly Lys Lys Leu Thr Gln Lys Leu Lys Glu Asp		
201	850	855	860
202	Ser Glu Ala Glu Ser Thr Glu Ser Val Pro Leu Val Cys Lys Ser Ala		
203	865	870	875
204	Ser Ala His Asn Leu Ser Ser Glu Lys Lys Thr Gly His Pro Arg Thr		
205	885	890	895

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206	Ser	Met	Leu	Gln	Lys	Ser	Leu	Ser	Val	Ile	Ala	Ser	Ala	Lys	Glu	Lys	
207			900						905					910			
208	Thr	Leu	Gly	Leu	Ala	Gly	Lys	Thr	Gln	Thr	Ala	Gly	Val	Glu	Glu	Arg	
209			915						920					925			
210	Thr	Lys	Ser	Gln	Lys	Pro	Leu	Pro	Lys	Asp	Lys	Glu	Thr	Asn	Arg	Asn	
211			930						935					940			
212	His	Ser	Asn	Ser	Asp	Asn	Thr	Glu	Thr	Lys	Asp	Pro	Ala	Pro	Gln	Asn	
213	945				950					955					960		
214	Ser	Asn	Pro	Ala	Glu	Glu	Pro	Arg	Lys	Pro	Gln	Lys	Ser	Gly	Ile	Met	
215					965					970					975		
216	Lys	Gln	Gln	Arg	Val	Asn	Pro	Thr	Thr	Ala	Asn	Ser	Asp	Leu	Asn	Pro	
217					980					985					990		
218	Gly	Thr	Thr	Gln	Met	Lys	Asp	Asn	Phe	Asp	Ile	Gly	Glu	Val	Cys	Pro	
219					995				1000					1005			
220	Trp	Glu	Val	Tyr	Asp	Leu	Thr	Pro	Gly	Pro	Val	Pro	Ser	Glu	Ser	Lys	
221					1010				1015					1020			
222	Val	Gln	Lys	His	Val	Ser	Ile	Val	Ala	Ser	Glu	Met	Glu	Lys	Asn	Pro	
223	1025					1030				1035					1040		
224	Thr	Phe	Ser	Leu	Lys	Glu	Lys	Ser	His	His	Lys	Pro	Lys	Ala	Ala	Glu	
225						1045				1050					1055		
226	Val	Cys	Gln	Gln	Ser	Asn	Gln	Lys	Arg	Ile	Asp	Lys	Ala	Glu	Val	Cys	
227						1060				1065					1070		
228	Leu	Trp	Glu	Ser	Gln	Gly	Gln	Ser	Ile	Leu	Glu	Asp	Glu	Lys	Leu	Leu	
229						1075				1080					1085		
230	Ile	Ser	Lys	Thr	Pro	Val	Leu	Pro	Glu	Arg	Ala	Lys	Glu	Glu	Asn	Gly	
231						1090				1095					1100		
232	Gly	Gln	Pro	Arg	Ala	Ala	Asn	Val	Cys	Ala	Gly	Gln	Ser	Glu	Glu	Leu	
233	1105					1110					1115					1120	
234	Pro	Pro	Lys	Ala	Ala	Ser	Lys	Thr	Glu	Asn	Glu	Asn	Leu	Asn	Gln		
235						1125				1130					1135		
236	Ile	Gly	His	Gln	Glu	Lys	Lys	Thr	Ser	Ser	Ser	Glu	Glu	Asn	Val	Arg	
237						1140				1145					1150		
238	Gly	Ser	Tyr	Asn	Ser	Ser	Asn	Asn	Phe	Gln	Gln	Pro	Leu	Thr	Ser	Arg	
239						1155				1160					1165		
240	Ala	Glu	Val	Cys	Pro	Trp	Glu	Phe	Glu	Thr	Pro	Ala	Gln	Pro	Asn	Ala	
241						1170				1175					1180		
242	Gly	Arg	Ser	Val	Ala	Leu	Pro	Ala	Ser	Ser	Ala	Leu	Ser	Ala	Asn	Lys	
243						1185				1190					1195	1200	
244	Ile	Ala	Gly	Pro	Arg	Lys	Glu	Glu	Ile	Trp	Asp	Ser	Phe	Lys	Val		
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249	<212>	TYPE:	DNA														
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255	aaggggaaagc	cgcacgcccc	gcagccgggt	cgagcccttg	cctcggactc	ctcggctccc									180		
256	tggagccgt	ccaccgatgg	caccatctg	gcccggaaaac	tccggaggg	gggtggccatg									240		

VERIFICATION SUMMARY

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Input Set : A:\LEX-0129-USA\SEQLIST.txt  
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L:13 M:270 C: Current Application Number differs, Replaced Current Application No  
L:13 M:271 C: Current Filing Date differs, Replaced Current Filing Date